

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

0978295.101504

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCCTG
AATCCCCCTTGTA TCTCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGTC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGT CAGAAGGAAGGATGGTGCAAATTAGCTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTGGTGAGCTCTTAGAACAAACACAGAAGAATT
GGTCCAGTTAAGTG CATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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FIGURE 131

CGGACGCGTGGGGGAAACCCCTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACCTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAAGTTGACCTACCCCTTGCACAC
CTACCCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCCTATCTGCAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTAAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT
TGTCCTCTCGGTGATGGTATGCTTTGGATTTGTTGTGCAACTGTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTTGTGGTTGTTAGATCTAAAACCTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATTCCACTCCTCATAGAGCTTTTAAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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